WHAT IS CLAIMED IS:

1. A method for identifying a test composition or agent which modulates the efficiency of translation termination which comprises:
   (a) contacting the MTT1 with a test composition or agent under conditions permitting binding between the MTT1 and the test composition;
   (b) detecting specific binding of the a test composition or agent to the MTT1; and
   (c) determining whether the a test composition or agent inhibits the MTT1 so as to identify a test composition or agent which is which modulates the efficiency of translation termination.

2. A method of identifying a test composition or agent which modulates binding to *MTT1*, the method comprising:
   (a) incubating components comprising the test composition, and *MTT1* wherein the incubating is carried out under conditions sufficient to permit the components to interact; and
   (b) measuring the effect of the test composition on the binding to *MTT1*.

3. The method of claim 2, further comprising identifying a gene comprising;
   (a) introducing into a cell a test composition which modulates binding to *MTT1*;
   (b) determining the phenotype of the cell after (a);
   (c) comparing the cellular phenotype after (a) with the cellular phenotype before (a); and
   (d) identifying the gene of the cell into which the test composition has been introduced.

4. A method of detecting a nonsense suppression disorder associated with the expression of mtt1 protein, wherein the method comprises contacting a sample from a subject having or suspected of having a disorder with a reagent that detects expression of the mtt1 protein and detecting the binding of the reagent in the sample.

5. An agent which inhibits, facilitates, or modulates the helicase, ATPase activity of MTT1.

6. The agent of claim 5, wherein the agent is a ribozyme, antisense molecule, or ligand which acts as an antagonist or agonist of translation termination.

7. An isolated multiprotein complex comprising a MTT1 gene, human Upf1p protein, a peptidyl eucaryotic release factor 1 (eRF1) and a peptidyl eucaryotic release factor 3 (eRF3), wherein the complex is effective to modulate peptidyl transferase activity during translation.

8. The complex of claim 7, further comprising human Upf3p and/or Upf2p.

9. An antibody which binds to the complex of claim 7.

10. The antibody of claim 9, wherein the antibody is a monoclonal or polyclonal

11. The antibody of claim 9, wherein the antibody has a label.

12. An agent which binds to the complex of claims 7 or 8.

13. An agent which inhibits or modulates the binding of human MTT1 to eRF3; or MTT1 ro a polysome.

14. An agent which facilitates the binding of human MTT1 to eRF3; or MTT1 ro a polysome.

15. The agent of claim 12, wherein the agent has a label or marker.

16. The agent of claim 14, wherein the agent is an antisense molecule or a ribozyme.

17. A method of modulating peptidyl transferase activity during translation, comprising contacting a cell with the complex of claim 7 in an amount effective to facilitate translation termination, thereby modulating the peptidyl transferase activity.

18. A method of modulating peptidyl transferase activity during translation, comprising contacting a cell with the agent of claim 12, in an amount effective to suppress nonsense translation termination, thereby modulating the peptidyl transferase activity.

19. The method of claim 18, wherein the peptidyl transferase activity during translation comprises initiation, elongation, termination and degradation of mRNA.

20. A method of modulating the efficiency of translation termination of mRNA at a nonsense codon and/or promoting degradation of abberant transcripts, comprising contacting a cell with the agent of claim 12, in an amount effective to modulate the efficiency of translation termination of mRNA at a nonsense codon and/or promoting degradation of abberant transcripts.

21. A method of screening for a drug involved in peptidyl transferase activity during translation comprising: a) contacting cells with a candidate drug; and b) assaying

for modulation of the complex of claims 7, wherein a drug that modulates complex is involved in peptidyl transferase activity.

22. A method of screening for a drug active involved in enhancing translation termination comprising: a) contacting cells with a candidate drug; and b) assaying for modulation of the protein complex of claims 7; wherein a drug that modulates protein complex is involved in enhancing translation termination.

23. A method of screening for a drug involved in enhancing translation termination comprising: a) incubating the drug and the complex; and b) measuring the effect on nonsense suppression, thereby screening for a drug involved in enhancing translation termination.

24. The method of claim 23, wherein the assay is a RNA assay or a ATPase assay.

25. A method of screening for a drug which inhibits the interaction between MTT1 and eRF3, comprising: a) contacting cells with a candidate drug; and b) assaying for modulation of the complex of claim 7, wherein a drug that modulates the binding of MTT1 to eRF3 is involved in enhancing translation termination.

26. A method of modulating the efficiency of translation termination of mRNA and/or degradation of abberant transcripts in a cell, said method comprising: a) providing a cell containing a vector comprising the nucleic acid encoding the complex of claim 7; or an antisense thereof; b) overexpressing said vector in said cell to produce an overexpressed complex so as to interfere with the function of the complex.

27. A method for identifying a disease state involving a defect in the complex of claim 7 comprising: (a) transfecting a cell with a nucleic acid which encodes the complex; (b) determining the proportion of the defective complex of the cell after

transfection; (c) comparing the proportion of the defective complex of the cell after transfection with the proportion of defective complex of the cell before transfection.

28. A method for treating a disease associated with peptidyl transferase activity, comprising administering to a subject a therapeutically effective amount of a pharmaceutical composition comprising the complex of claim 7 or the agent of claim 12, and a pharmaceutical carrier or diluent, thereby treating the subject.

29. The method of claim 28, wherein the disease results from a nonsense or frameshift mutation.

30. The method of claim 29, wherein the disease is β-thalassemia, β-globin, Duchenne/Becker Muscular Dystrophy, Hemophilia A, Hemophilia B, Von Willebrand Disease, Osteogenesis Imperfecta (OI), Breast cancer, Ovarian Cancer, Wilms Tumor, Hirschsprung disease, Cystic fibrosis, Kidney Stones, Familial hypercholesterolemia (FH), Retinitis Pigmentosa, or Neurofibromatosis, Retinoblastoma, ATM, Costmann Disease.

31. A method for identifying a disease state involving defective multimeric proteins comprising:

(a) transfecting a cell with the vector of claim ;

(b) determining the proportion of defective multimeric proteins of the cell after tansfection;

(c) comparing the proportion of defective multimeric proteins of the cell after transfection with the proportion of defective multimeric proteins of the cell before transfection.

32. A method of identifying genes which are involved in modulation of translation termination, which comprises: a) isolated a gene of interest; and b) determining

whether the gene of interest comprises motifs I-IX, wherein if the gene comprises any one of the nine motifs the gene modulates translation fidelity including iniatiatioin, elongation, termination, termination, decay.

33. The method of claim 32, wherein the motif I comprises the sequence: GppGTKTxT-X(n).

34. The method of claim 32, wherein the motif II comprises the sequence riLxcaSNxAvDxl-X(n).

35. The method of claim 32, wherein the motif III comprises the sequence vviDExxQaxxxxxiPi- X(n).

36. The method of claim 32, wherein the motif IV comprises the sequence xxi1 aGDxxQLp- X(n).

37. The method of claim 32, wherein the motif V comprises the sequence lxx SLF erv- X(n).

38. The method of claim 32, wherein the motif VI comprises the sequence LxxQYRMhpxisefpxYxgxL- X(n).

39. The method of claim 32, wherein the motif VII comprises the sequence IgvitPYxxQvxxl- X(n).

40. The method of claim 32, wherein the motif VIII comprises the sequence vevxtVDxFQGreKdxIilSc VR- X(n).

41. The method of claim 32, wherein the motif IX comprises the sequence iGFLxdxRRINValTRak.